

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/019,04813
Source: IFW/6
Date Processed by STIC: 08/01/2006

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 08/01/2006

PATENT APPLICATION: US/10/019,048B

TIME: 10:10:49

Input Set : A:\00930032.APP

Output Set: N:\CRF4\08012006\J019048B.raw

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3 <110> APPLICANT: HEINZ, ERNST
4     GIRKE, THOMAS
5     SCHEFFLER, JODI
6     SILVA, OSWALDO DA COSTA E
8 <120> TITLE OF INVENTION: PLANTS EXPRESSING DELTA-6-DESATURASE GENES,
9     PUFAS-CONTAINING OILS FROM THESE PLANTS, AND A PROCESS
10    FOR THE PREPARATION OF UNSATURATED FATTY ACIDS
12 <130> FILE REFERENCE: 0093/000032
14 <140> CURRENT APPLICATION NUMBER: 10/019,048B
15 <141> CURRENT FILING DATE: 2001-12-27
17 <150> PRIOR APPLICATION NUMBER: DE 10030976.3
18 <151> PRIOR FILING DATE: 2000-06-03
20 <150> PRIOR APPLICATION NUMBER: 09/347,531
21 <151> PRIOR FILING DATE: 1999-07-06
23 <160> NUMBER OF SEQ ID NOS: 13
25 <170> SOFTWARE: PatentIn Ver. 3.3
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 2012
29 <212> TYPE: DNA
30 <213> ORGANISM: Physcomitrella patens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (319)..(1896)
36 <400> SEQUENCE: 1
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41 tacctccggg ttttggagcg ggcaaactct gttgcggctc ggaaggctat aggttcggca 180
43 ggagactgtt gattttatgt cgggggcatt gccattgttg agagcggggg agactcagga 240
45 tctgtgagtg tgcgtgcagc gcccgcactg ccgcagagcg tctgtgtatg acgaggttgt 300
47 tgtggagcgg cttttgaa atg gta ttc gcg ggc ggt gga ctt cag cag ggc 351
48                               Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly
49                               1           5           10
51 tct ctc gaa gaa aac atc gac gtc gag cac att gcc agt atg tct ctc 399
52 Ser Leu Glu Glu Asn Ile Asp Val Glu His Ile Ala Ser Met Ser Leu
53           15           20           25
55 ttc agc gac ttc ttc agt tat gtg tct tca act gtt ggt tcg tgg agc 447
56 Phe Ser Asp Phe Phe Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser
57           30           35           40
59 gta cac agt ata caa cct ttg aag cgc ctg acg agt aag aag cgt gtt 495
60 Val His Ser Ile Gln Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val
61           45           50           55
63 tcg gaa agc gct gcc gtg caa tgt ata tca gct gaa gtt cag aga aat 543
64 Ser Glu Ser Ala Ala Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn

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65	60				65				70				75				
67	tcg	agt	acc	cag	gga	act	gcg	gag	gca	ctc	gca	gaa	tca	gtc	gtg	aag	591
68	Ser	Ser	Thr	Gln	Gly	Thr	Ala	Glu	Ala	Leu	Ala	Glu	Ser	Val	Val	Lys	
69						80				85				90			
71	ccc	acg	aga	cga	agg	tca	tct	cag	tgg	aag	aag	tcg	aca	cac	ccc	cta	639
72	Pro	Thr	Arg	Arg	Arg	Ser	Ser	Gln	Trp	Lys	Lys	Ser	Thr	His	Pro	Leu	
73						95				100				105			
75	tca	gaa	gta	gca	gta	cac	aac	aag	cca	agc	gat	tgc	tgg	att	gtt	gta	687
76	Ser	Glu	Val	Ala	Val	His	Asn	Lys	Pro	Ser	Asp	Cys	Trp	Ile	Val	Val	
77						110				115				120			
79	aaa	aac	aag	gtg	tat	gat	gtt	tcc	aat	ttt	gcg	gac	gag	cat	ccc	gga	735
80	Lys	Asn	Lys	Val	Tyr	Asp	Val	Ser	Asn	Phe	Ala	Asp	Glu	His	Pro	Gly	
81						125				130				135			
83	gga	tca	gtt	att	agt	act	tat	ttt	gga	cga	gac	ggc	aca	gat	gtt	ttc	783
84	Gly	Ser	Val	Ile	Ser	Thr	Tyr	Phe	Gly	Arg	Asp	Gly	Thr	Asp	Val	Phe	
85	140					145				150				155			
87	tct	agt	ttt	cat	gca	gct	tct	aca	tgg	aaa	att	ctt	caa	gac	ttt	tac	831
88	Ser	Ser	Phe	His	Ala	Ala	Ser	Thr	Trp	Lys	Ile	Leu	Gln	Asp	Phe	Tyr	
89						160				165				170			
91	att	ggt	gac	gtg	gag	agg	gtg	gag	ccg	act	cca	gag	ctg	ctg	aaa	gat	879
92	Ile	Gly	Asp	Val	Glu	Arg	Val	Glu	Pro	Thr	Pro	Glu	Leu	Leu	Lys	Asp	
93						175				180				185			
95	ttc	cga	gaa	atg	aga	gct	ctt	ttc	ctg	agg	gag	caa	ctt	ttc	aaa	agt	927
96	Phe	Arg	Glu	Met	Arg	Ala	Leu	Phe	Leu	Arg	Glu	Gln	Leu	Phe	Lys	Ser	
97						190				195				200			
99	tcg	aaa	ttg	tac	tat	gtt	atg	aag	ctg	ctc	acg	aat	gtt	gct	att	ttt	975
100	Ser	Lys	Leu	Tyr	Tyr	Val	Met	Lys	Leu	Leu	Thr	Asn	Val	Ala	Ile	Phe	
101						205				210				215			
103	gct	gcg	agc	att	gca	ata	ata	tgt	tgg	agc	aag	act	att	tca	gcg	gtt	1023
104	Ala	Ala	Ser	Ile	Ala	Ile	Ile	Cys	Trp	Ser	Lys	Thr	Ile	Ser	Ala	Val	
105	220					225				230				235			
107	ttg	gct	tca	gct	tgt	atg	atg	gct	ctg	tgt	ttc	caa	cag	tgc	gga	tgg	1071
108	Leu	Ala	Ser	Ala	Cys	Met	Met	Ala	Leu	Cys	Phe	Gln	Gln	Cys	Gly	Trp	
109						240				245				250			
111	cta	tcc	cat	gat	ttt	ctc	cac	aat	cag	gtg	ttt	gag	aca	cgc	tgg	ctt	1119
112	Leu	Ser	His	Asp	Phe	Leu	His	Asn	Gln	Val	Phe	Glu	Thr	Arg	Trp	Leu	
113						255				260				265			
115	aat	gaa	gtt	gtc	ggg	tat	gtg	atc	ggc	aac	gcc	gtt	ctg	ggg	ttt	agt	1167
116	Asn	Glu	Val	Gly	Tyr	Val	Ile	Gly	Asn	Ala	Val	Leu	Gly	Phe	Ser		
117						270				275				280			
119	aca	ggg	tgg	tgg	aag	gag	aag	cat	aac	ctt	cat	cat	gct	gct	cca	aat	1215
120	Thr	Gly	Trp	Trp	Lys	Glu	Lys	His	Asn	Leu	His	His	Ala	Ala	Pro	Asn	
121						285				290				295			
123	gaa	tgc	gat	cag	act	tac	caa	cca	att	gat	gaa	gat	att	gat	act	ctc	1263
124	Glu	Cys	Asp	Gln	Thr	Tyr	Gln	Pro	Ile	Asp	Glu	Asp	Ile	Asp	Thr	Leu	
125	300					305				310				315			
127	ccc	ctc	att	gcc	tgg	agc	aag	gac	ata	ctg	gcc	aca	gtt	gag	aat	aag	1311
128	Pro	Leu	Ile	Ala	Trp	Ser	Lys	Asp	Ile	Leu	Ala	Thr	Val	Glu	Asn	Lys	
129						320				325				330			

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131 aca ttc ttg cga atc ctc caa tac cag cat ctg ttc ttc atg ggt ctg 1359
132 Thr Phe Leu Arg Ile Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu
133      335      340      345
135 tta ttt ttc gcc cgt ggt agt tgg ctc ttt tgg agc tgg aga tat acc 1407
136 Leu Phe Phe Ala Arg Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr
137      350      355      360
139 tct aca gca gtg ctc tca cct gtc gac agg ttg ttg gag aag gga act 1455
140 Ser Thr Ala Val Leu Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr
141      365      370      375
143 gtt ctg ttt cac tac ttt tgg ttc gtc ggg aca gcg tgc tat ctt ctc 1503
144 Val Leu Phe His Tyr Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu
145 380      385      390      395
147 cct ggt tgg aag cca tta gta tgg atg gcg gtg act gag ctc atg tcc 1551
148 Pro Gly Trp Lys Pro Leu Val Trp Met Ala Val Thr Glu Leu Met Ser
149      400      405      410
151 ggc atg ctg ctg ggc ttt gta ttt gta ctt agc cac aat ggg atg gag 1599
152 Gly Met Leu Leu Gly Phe Val Phe Val Leu Ser His Asn Gly Met Glu
153      415      420      425
155 gtt tat aat tcg tct aaa gaa ttc gtg agt gca cag atc gta tcc aca 1647
156 Val Tyr Asn Ser Ser Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr
157      430      435      440
159 cgg gat atc aaa gga aac ata ttc aac gac tgg ttc act ggt ggc ctt 1695
160 Arg Asp Ile Lys Gly Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu
161      445      450      455
163 aac agg caa ata gag cat cat ctt ttc cca aca atg ccc agg cat aat 1743
164 Asn Arg Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn
165 460      465      470      475
167 tta aac aaa ata gca cct aga gtg gag gtg ttc tgt aag aaa cac ggt 1791
168 Leu Asn Lys Ile Ala Pro Arg Val Glu Val Phe Cys Lys Lys His Gly
169      480      485      490
171 ctg gtg tac gaa gac gta tct att gct acc ggc act tgc aag gtt ttg 1839
172 Leu Val Tyr Glu Asp Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu
173      495      500      505
175 aaa gca ttg aag gaa gtc gcg gag gct gcg gca gag cag cat gct acc 1887
176 Lys Ala Leu Lys Glu Val Ala Glu Ala Ala Glu Gln His Ala Thr
177      510      515      520
179 acc agt taa cagtctttgg aaagcttggc aattgatctt tattctccac 1936
180 Thr Ser
181      525
183 ggcagttgct tgtttgtttt ggggtgaatg accgaatgta ctggcatcca ttcttctgta 1996
185 gccatcaatt ttgaac 2012
188 <210> SEQ ID NO: 2
189 <211> LENGTH: 525
190 <212> TYPE: PRT
191 <213> ORGANISM: Physcomitrella patens
193 <400> SEQUENCE: 2
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197 Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe

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198          20          25          30
200 Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln
201          35          40          45
203 Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala
204          50          55          60
206 Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly
207 65          70          75          80
209 Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg
210          85          90          95
212 Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val
213          100          105          110
215 His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr
216          115          120          125
218 Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser
219          130          135          140
221 Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala
222 145          150          155          160
224 Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu
225          165          170          175
227 Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg
228          180          185          190
230 Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr
231          195          200          205
233 Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala
234          210          215          220
236 Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys
237 225          230          235          240
239 Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe
240          245          250          255
242 Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly
243          260          265          270
245 Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys
246          275          280          285
248 Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr
249          290          295          300
251 Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp
252 305          310          315          320
254 Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile
255          325          330          335
257 Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg
258          340          345          350
260 Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu
261          355          360          365
263 Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr
264          370          375          380
266 Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro
267 385          390          395          400
269 Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly
270          405          410          415

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272 Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser
273           420           425           430
275 Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly
276           435           440           445
278 Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu
279           450           455           460
281 His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala
282 465           470           475           480
284 Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp
285           485           490           495
287 Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu
288           500           505           510
290 Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser
291           515           520           525
295 <210> SEQ ID NO: 3
296 <211> LENGTH: 6
297 <212> TYPE: PRT
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
302     peptide
304 <400> SEQUENCE: 3
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306   1           5
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310 <211> LENGTH: 20
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
316     oligonucleotide
318 <220> FEATURE:
319 <221> NAME/KEY: modified_base
320 <222> LOCATION: (15)
321 <223> OTHER INFORMATION: Inosine
323 <400> SEQUENCE: 4
W--> 324 tgggtggaart ggamncayaa           20
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328 <211> LENGTH: 17
329 <212> TYPE: DNA
330 <213> ORGANISM: Artificial Sequence
332 <220> FEATURE:
333 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
334     oligonucleotide
336 <220> FEATURE:
337 <221> NAME/KEY: modified_base
338 <222> LOCATION: (6)
339 <223> OTHER INFORMATION: a, c, g, or t
341 <400> SEQUENCE: 5

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/01/2006
PATENT APPLICATION: US/10/019,048B TIME: 10:10:50

Input Set : A:\00930032.APP
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 15
Seq#:5; N Pos. 6

VERIFICATION SUMMARY

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L:324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0

L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0